

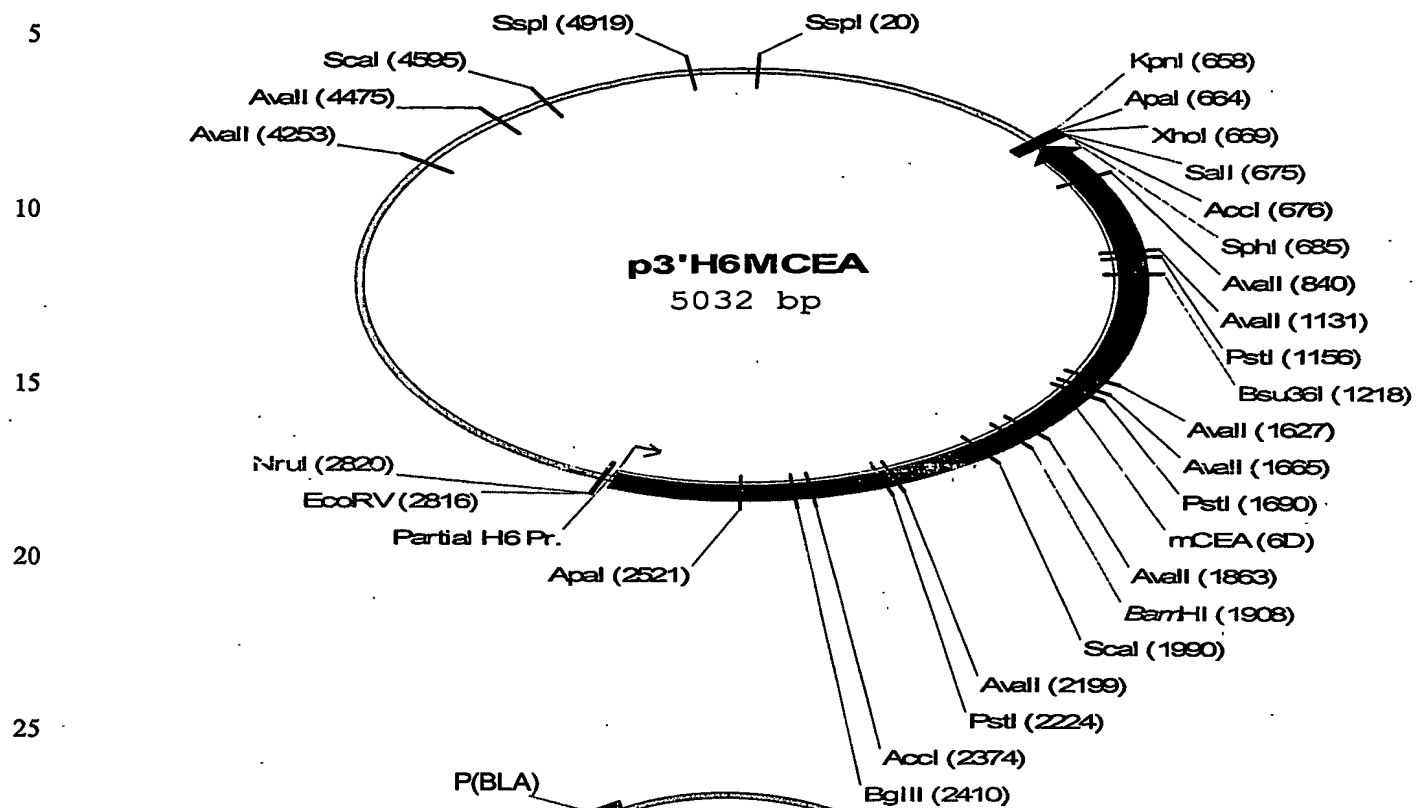
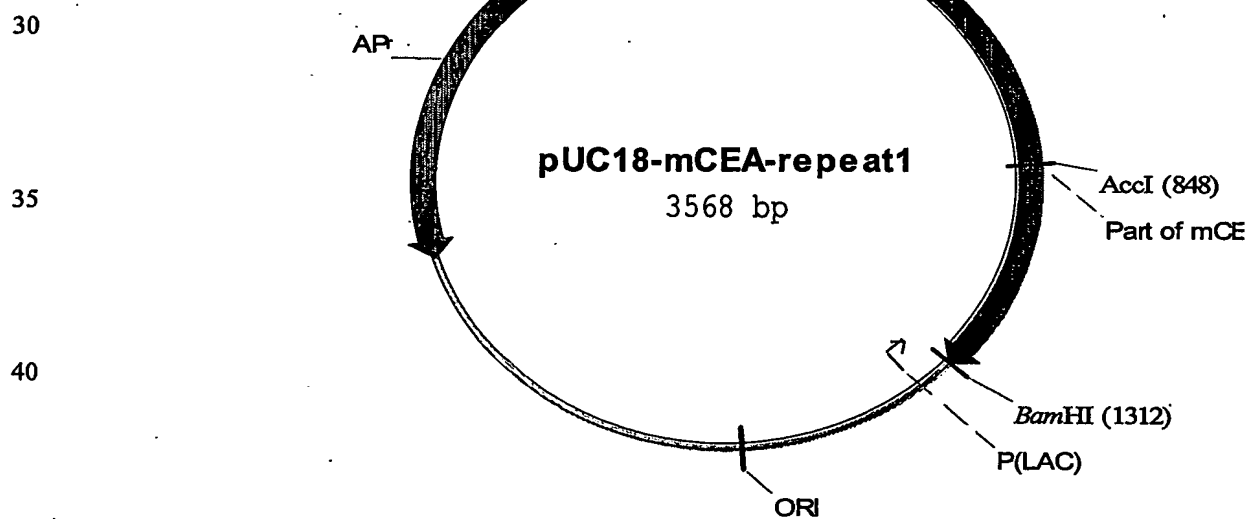
FIGURE 1**A.****B.**

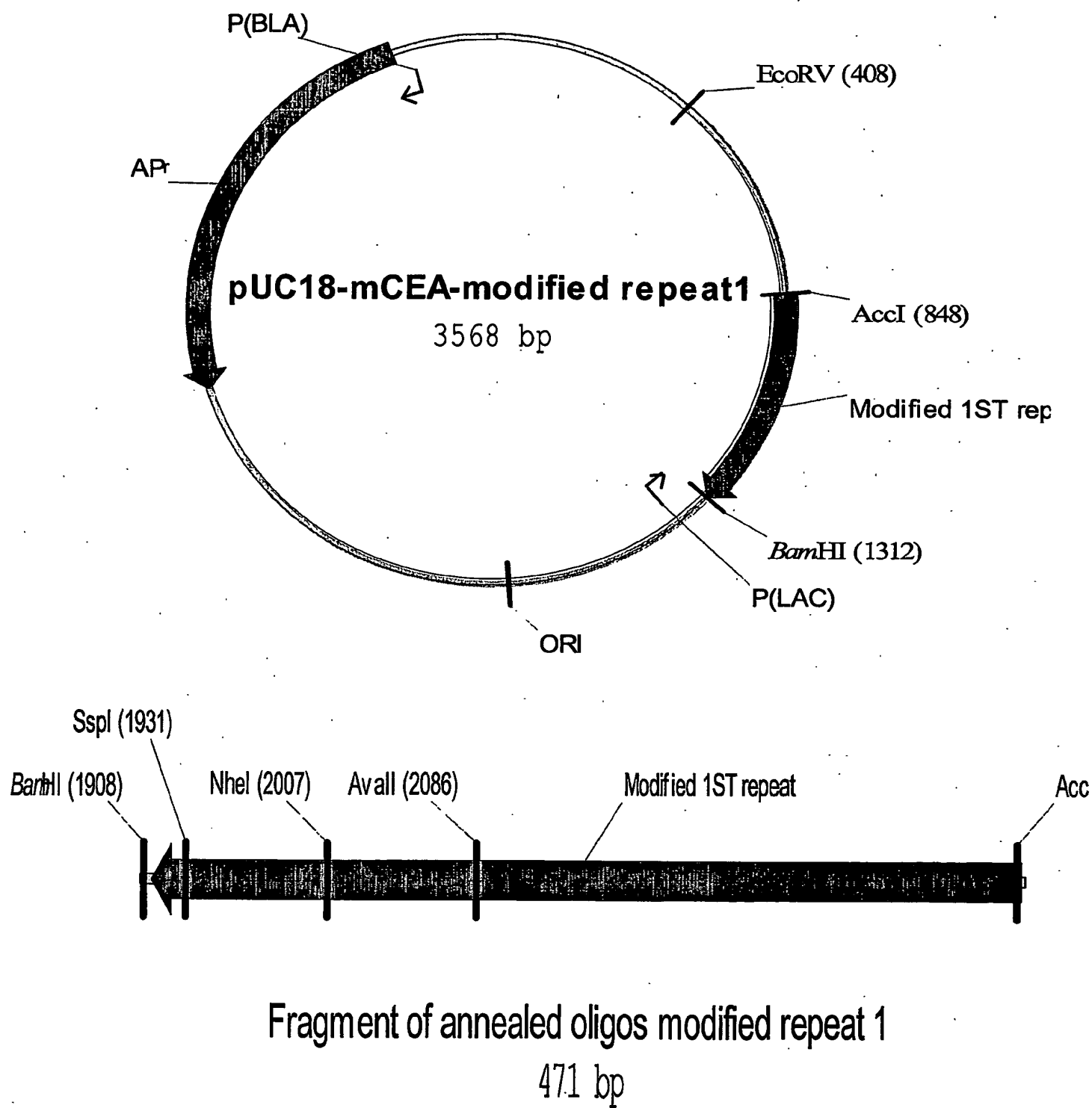
FIGURE 2

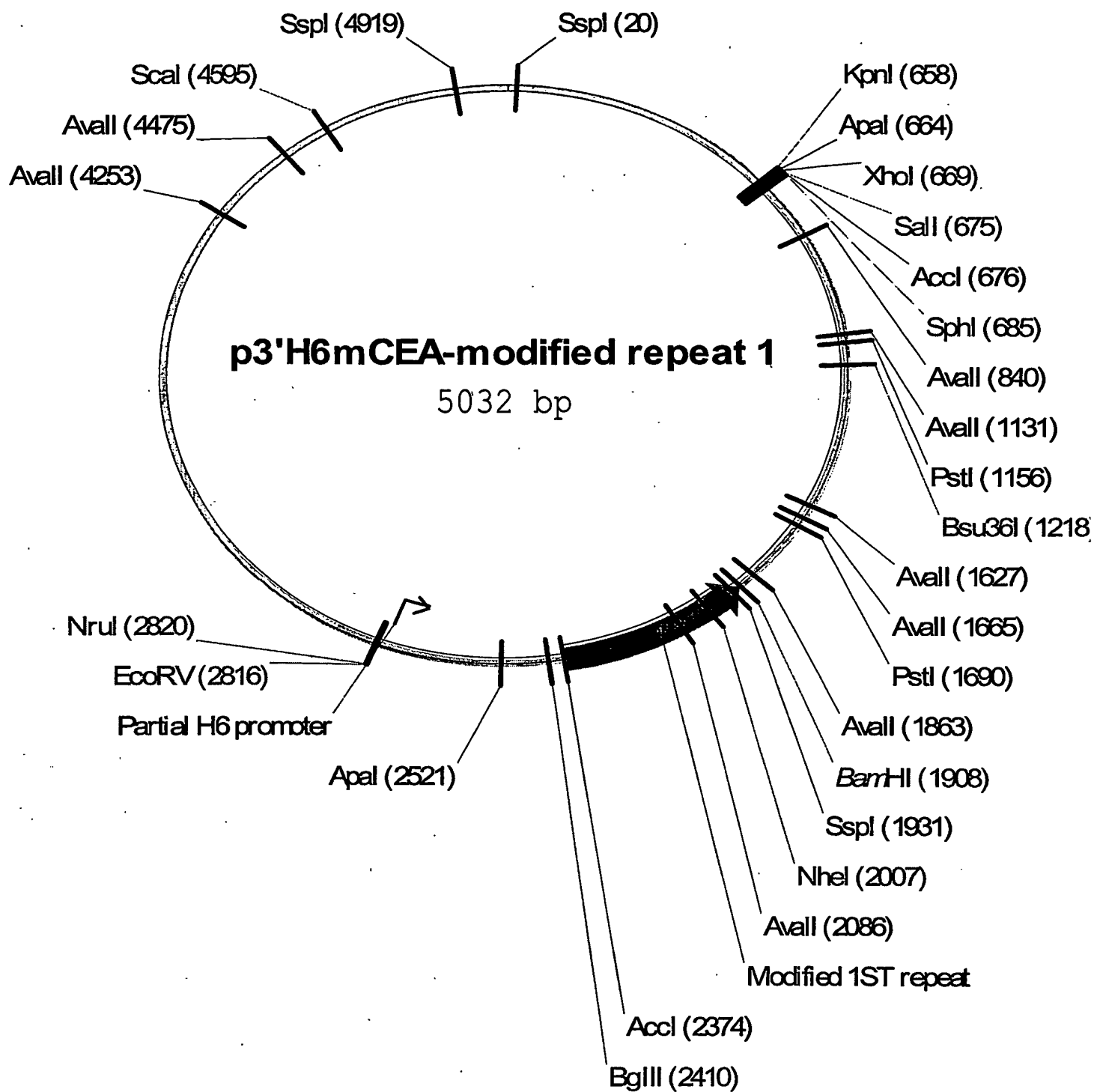
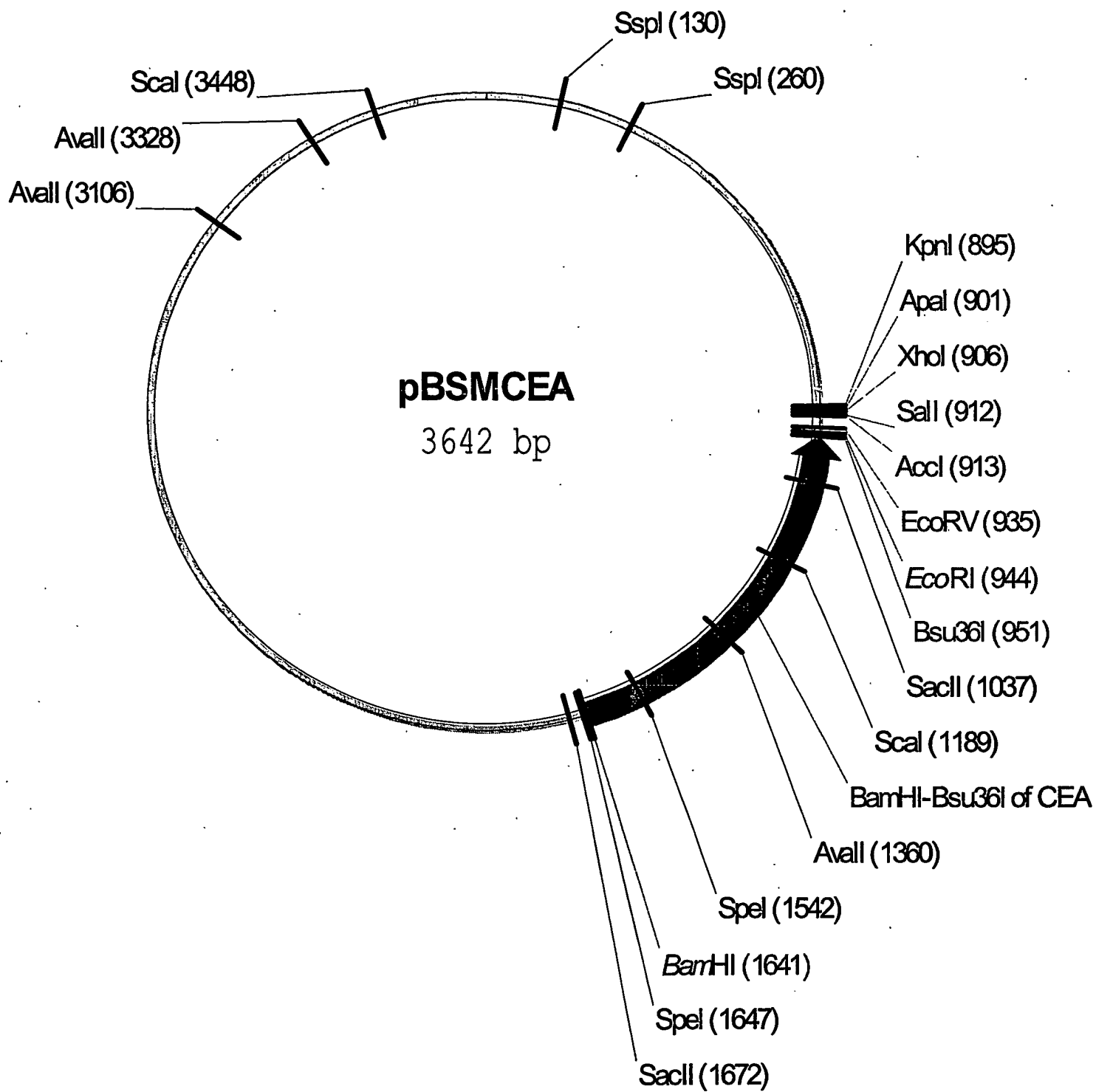
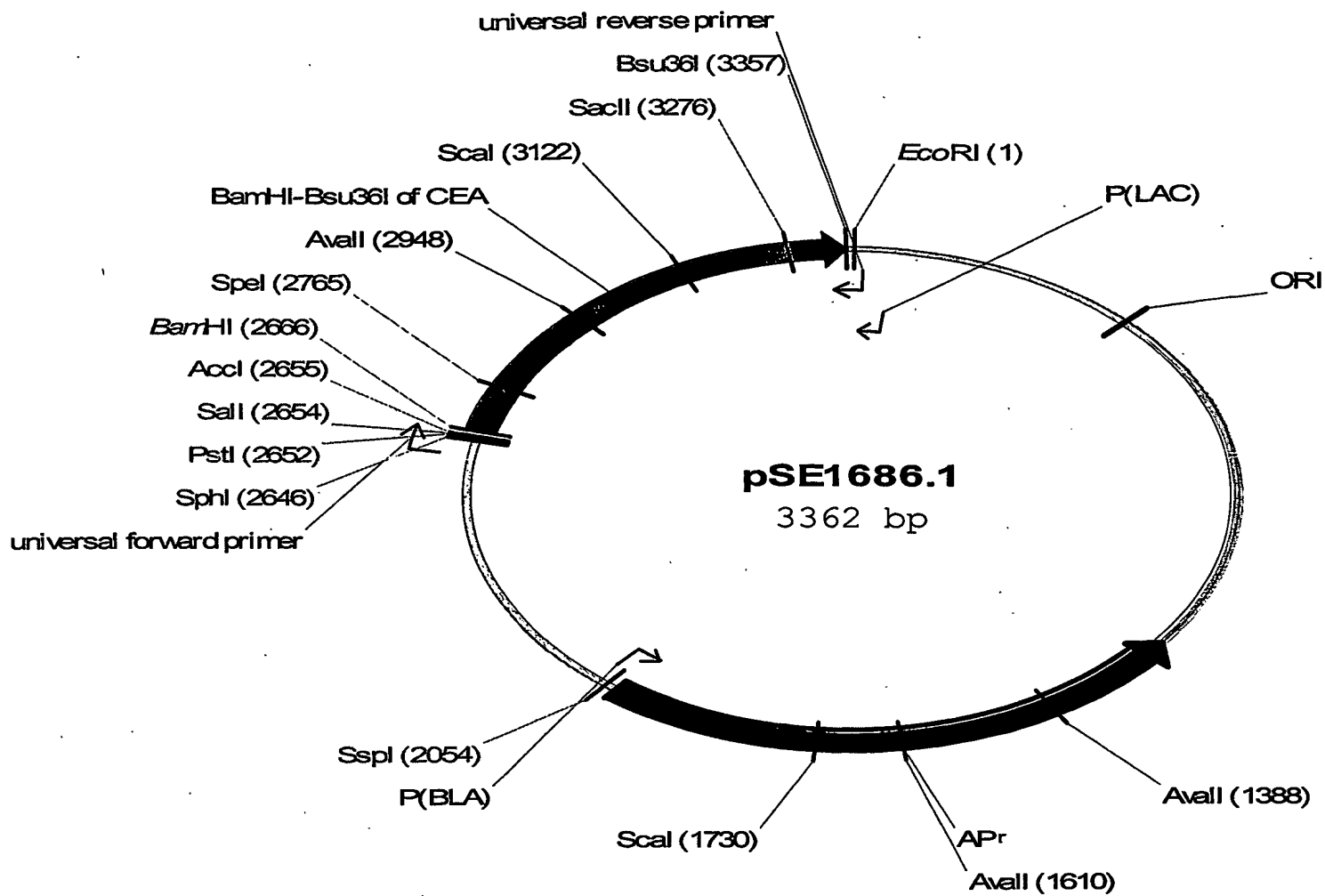
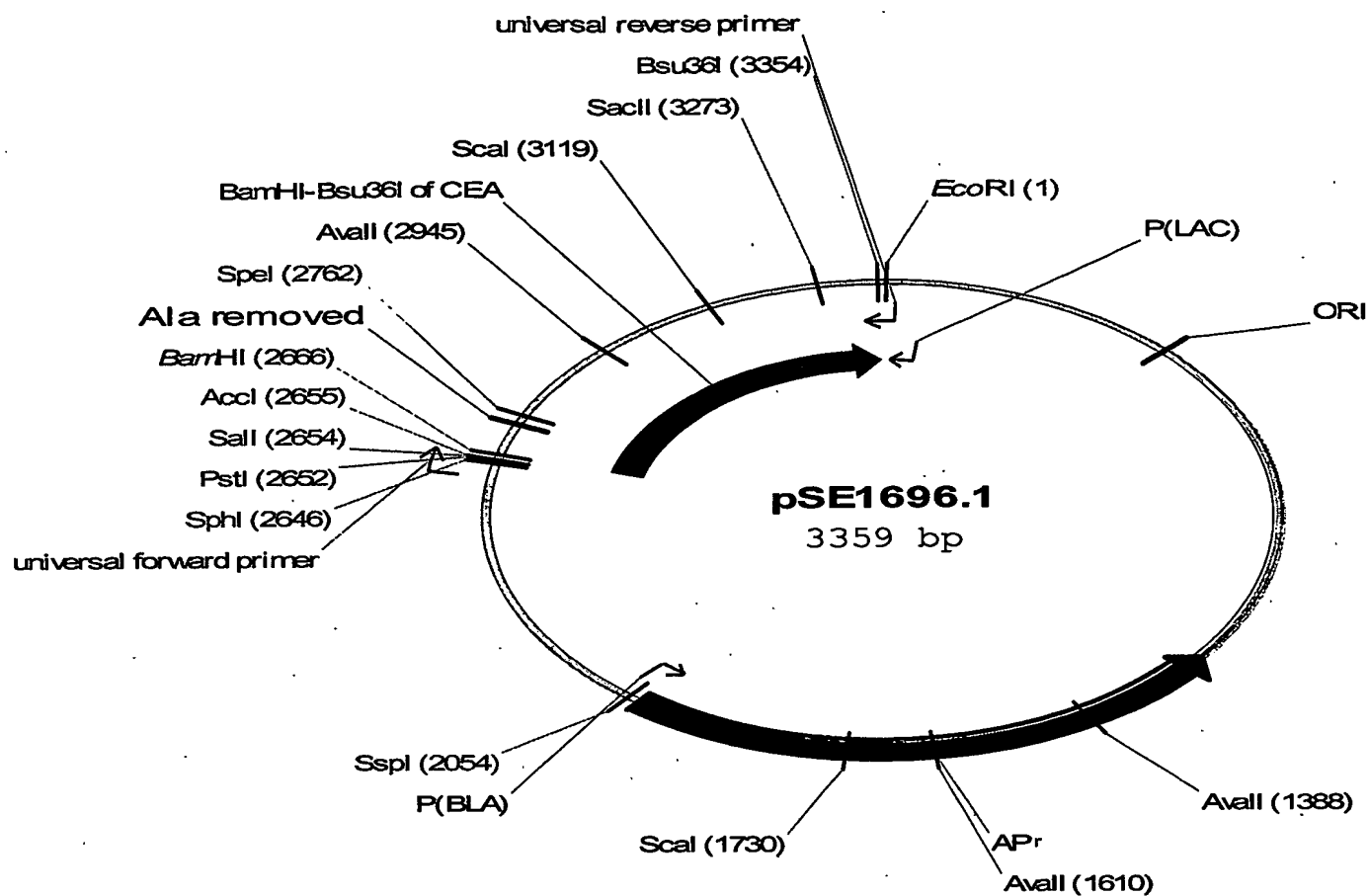
FIGURE 3

FIGURE 4

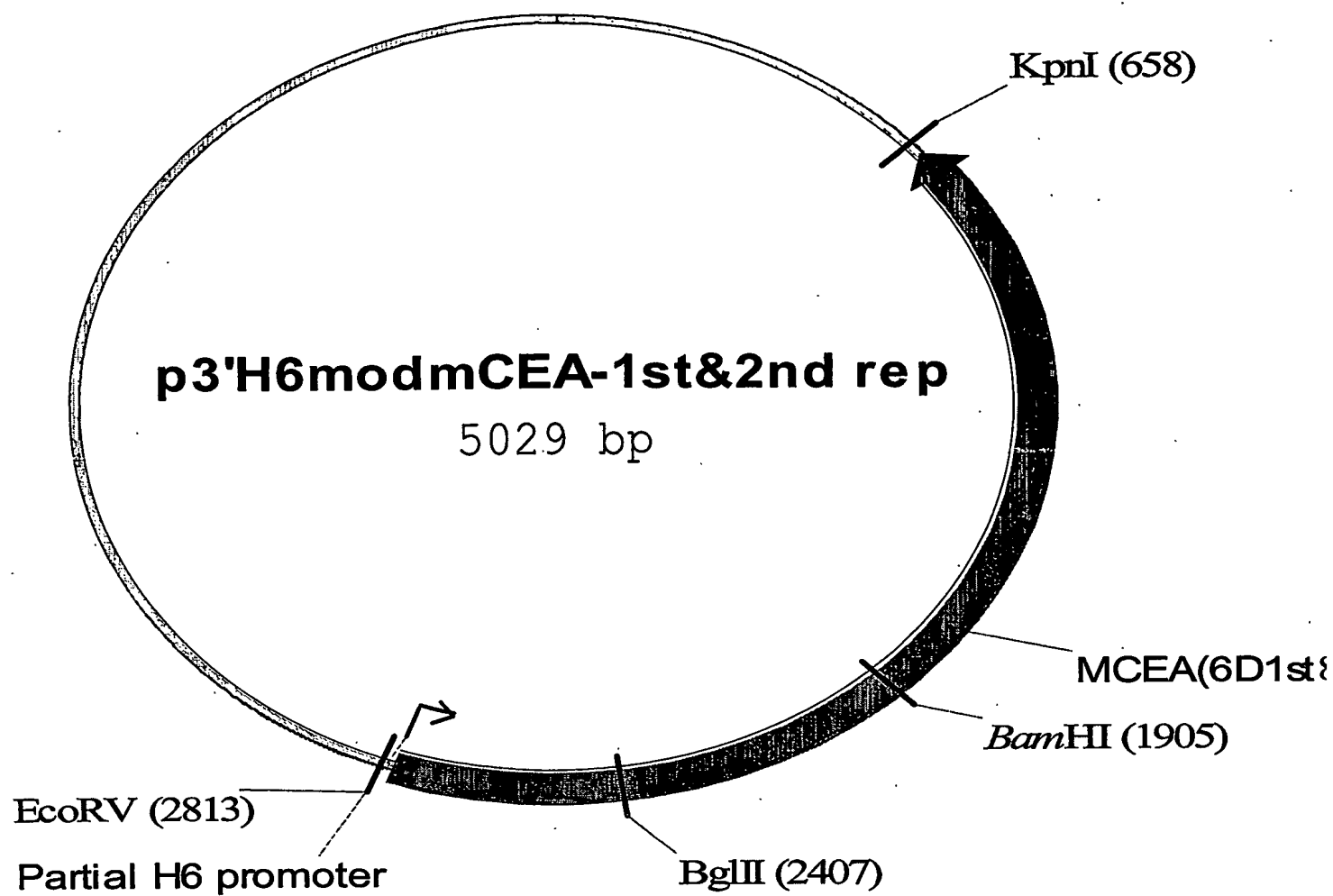
5/29

FIGURE 5**pUC18 mCEA modified repeat 2 (gsoe)**

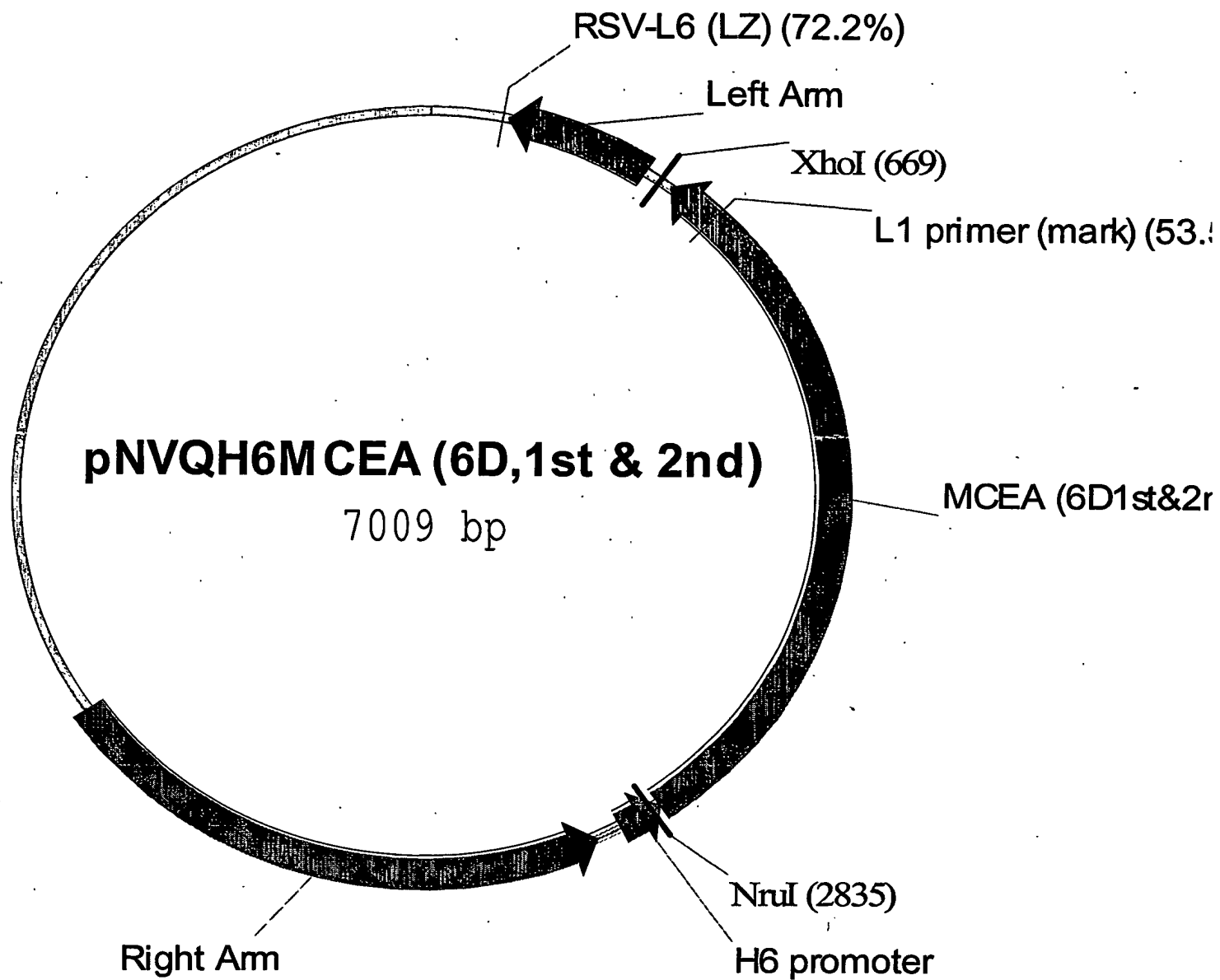
6/29

FIGURE 6

pUC18 mCEA modified repeat 2 gsoe minus Ala

FIGURE 7

8/29

FIGURE 8

9/29

FIGURE 9A

		1				50
	mCEA (6D)	ATGGAGTCTC	CCTCGGCCCC	TCCCCACAGA	TGGTGCATCC	CCTGGCAGAG
5	mCEA (6D, 1st&2nd)	ATGGAGTCTC	CCTCGGCCCC	TCCCCACAGA	TGGTGCATCC	CCTGGCAGAG
		51				100
	mCEA (6D)	GCTCCTGCTC	ACAGCCTCAC	TTCTAACCTT	CTGGAACCCG	CCCACCACTG
10	mCEA (6D, 1st&2nd)	GCTCCTGCTC	ACAGCCTCAC	TTCTAACCTT	CTGGAACCCG	CCCACCACTG
		101				150
	mCEA (6D)	CCAAGCTCAC	TATTGAATCC	ACGCCGTTCA	ATGTCGCAGA	GGGGAAGGAG
	mCEA (6D, 1st&2nd)	CCAAGCTCAC	TATTGAATCC	ACGCCGTTCA	ATGTCGCAGA	GGGGAAGGAG
15		151				200
	mCEA (6D)	GTGCTTCTAC	TTGTCCACAA	TCTGCCCCAG	CATCTTTTTG	GCTACAGCTG
	mCEA (6D, 1st&2nd)	GTGCTTCTAC	TTGTCCACAA	TCTGCCCCAG	CATCTTTTTG	GCTACAGCTG
		201				250
20	mCEA (6D)	GTACAAAGGT	GAAAGAGTGG	ATGGCAACCG	TCAAATTATA	GGATATGTAA
	mCEA (6D, 1st&2nd)	GTACAAAGGT	GAAAGAGTGG	ATGGCAACCG	TCAAATTATA	GGATATGTAA
		251				300
25	mCEA (6D)	TAGGAACTCA	ACAAGCTACC	CCAGGGCCCG	CATACAGTGG	TCGAGAGATA
	mCEA (6D, 1st&2nd)	TAGGAACTCA	ACAAGCTACC	CCAGGGCCCG	CATACAGTGG	TCGAGAGATA
		301				350
	mCEA (6D)	ATATACCCCA	ATGCATCCCT	GCTGATCCAG	AACATCATCC	AGAATGACAC
30	mCEA (6D, 1st&2nd)	ATATACCCCA	ATGCATCCCT	GCTGATCCAG	AACATCATCC	AGAATGACAC
		351				400
	mCEA (6D)	AGGATTCTAC	ACCCTACACG	TCATAAAGTC	AGATCTTGTG	AATGAAGAAG
	mCEA (6D, 1st&2nd)	AGGATTCTAC	ACCCTACACG	TCATAAAGTC	AGATCTTGTG	AATGAAGAAG
35		401				450
	mCEA (6D)	CAACTGGCCA	GTTCCGGGTA	TACCCGGAGC	TGCCCAAGCC	CTCCATCTCC
	mCEA (6D, 1st&2nd)	CAACTGGCCA	GTTCCGGGTA	TACCCGGAAC	TCCCTAAGCC	TTCTATTAGC
		451				500
40	mCEA (6D)	AGCAACAAC	CCAAACCCGT	GGAGGACAAG	GATGCTGTGG	CCTTCACCTG
	mCEA (6D, 1st&2nd)	<u>TCCAATAATA</u>	<u>GTAAGCCTGT</u>	<u>CGAAGACAAA</u>	<u>GATGCCGTCG</u>	<u>CTTTTACATG</u>
		501				550
45	mCEA (6D)	TGAACCTGAG	ACTCAGGACG	CAACCTACCT	GTGGTGGGTA	AACAATCAGA
	mCEA (6D, 1st&2nd)	<u>CGAGCCCGAA</u>	<u>ACTCAAGACG</u>	<u>CAACATATCT</u>	<u>CTGGTGGGTG</u>	<u>AACAACCACT</u>
		551				600
	mCEA (6D)	GCCTCCCGGT	CAGTCCCAGG	CTGCAGCTGT	CCAATGGCAA	CAGGACCCTC
50	mCEA (6D, 1st&2nd)	<u>CCCTGCCTGT</u>	<u>GTCCCTTAGA</u>	<u>CTCCAACCTCA</u>	<u>GCAACGGAAA</u>	<u>TAGAACTCTG</u>
		601				650
	mCEA (6D)	ACTCTATTCA	ATGTCACAAG	AAATGACACA	GCAAGCTACA	AATGTGAAAC
	mCEA (6D, 1st&2nd)	<u>ACCCTGTTTA</u>	<u>ACGTGACCAG</u>	<u>GAACGACACA</u>	<u>GCAAGCTACA</u>	<u>AATGCGAAAC</u>

10/29

FIGURE 9B

		651				700
	mCEA (6D)	CCAGAACCCA	GTGAGTGCCA	GGCGCAGTGA	TTCAGTCATC	CTGAATGTCC
5	mCEA (6D, 1st&2nd)	CCAAAATCCA	GTCAGCGCCA	GGAGGTCTGA	TTCAGTGATT	CTCAACGTGC
		701				750
	mCEA (6D)	TCTATGGCCC	GGATGCCCCC	ACCATTTCCC	CTCTAAACAC	ATCTTACAGA
	mCEA (6D, 1st&2nd)	TTTACGGACC	CGATGCTCCT	ACAATCAGCC	CTCTAAACAC	AAGCTATAGA
10		751				800
	mCEA (6D)	TCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	ACCCACCTGC
	mCEA (6D, 1st&2nd)	TCAGGGGAAA	ATCTGAATCT	GAGCTGTCAT	GCCGCTAGCA	ATCCTCCCGC
		801				850
15	mCEA (6D)	ACAGTACTCT	TGGTTTGTCA	ATGGGACTTT	CCAGCAATCC	ACCCAAGAGC
	mCEA (6D, 1st&2nd)	CCAATACAGC	TGGTTTGTCA	ATGGCACTTT	CCAACAGTCC	ACCCAGGAAC
		851				900
20	mCEA (6D)	TCTTTATCCC	CAACATCACT	GTGAATAATA	GTGGATCCTA	TACGTGCCAA
	mCEA (6D, 1st&2nd)	TGTTCAATCC	CAATATTACC	GTGAACAATA	GTGGATCCTA	CACGTGCCAA
		901				950
25	mCEA (6D)	GCCCATAACT	CAGACACTGG	CCTCAATAGG	ACCACAGTCA	CGACGATCAC
	mCEA (6D, 1st&2nd)	GCTCACAATA	GCGACACCGG	ACTCAACCGC	ACAACCGTGA	CGACGATTAC
		951				1000
	mCEA (6D)	AGTCTATGAG	CCACCCAAAC	CCTTCATCAC	CAGCAACAAC	TCCAACCCCG
	mCEA (6D, 1st&2nd)	CGTGTATGAG	CCACCAAAC	CATTCAATAC	TAGTAACAAT	TCTAACCCAG
30		1001				1050
	mCEA (6D)	TGGAGGATGA	GGATGCTGTA	GCCTTAACCT	GTGAACCTGA	GATTCAGAAC
	mCEA (6D, 1st&2nd)	TTGAGGATGA	GGACGCAGTT	GCATTAACCT	GTGAGCCAGA	GATTCAAAAT
		1051				1100
35	mCEA (6D)	ACAACCTACC	TGTGGTGGGT	AAATAATCAG	AGCCTCCCGG	TCAGTCCCAG
	mCEA (6D, 1st&2nd)	ACCACTTATT	TATGGTGGGT	CAATAACCAA	AGTTTGCCGG	TTAGCCCACG
		1101				1150
40	mCEA (6D)	GCTGCAGCTG	TCCAATGACA	ACAGGACCCT	CACTCTACTC	AGTGTACAA
	mCEA (6D, 1st&2nd)	CTTGCAGTTG	TCTAATGATA	ACCGCACATT	GACACTCCTG	TCCGTTACTC
		1151				1200
45	mCEA (6D)	GGAATGATGT	AGGACCCTAT	GAGTGTGGAA	TCCAGAACGA	ATTAAGTGTT
	mCEA (6D, 1st&2nd)	GCAATGATGT	AGGACCTTAT	GAGTGTGGCA	TTCAGAATGA	ATTATCCGTT
		1201				1250
	mCEA (6D)	GACCACAGCG	ACCCAGTCAT	CCTGAATGTC	CTCTATGGCC	CAGACGACCC
	mCEA (6D, 1st&2nd)	GATCACTCCG	ACCCGTGTAT	CCTTAATGTT	TTGTATGGCC	CAGACGACCC
50		1251				1300
	mCEA (6D)	CACCATTTCC	CCCTCATACA	CCTATTACCG	TCCAGGGGTG	AACCTCAGCC
	mCEA (6D, 1st&2nd)	AACTATATCT	CCATCATACA	CCTACTACCG	TCCCGGCGTG	AACCTGAGCC

11/29

FIGURE 9C

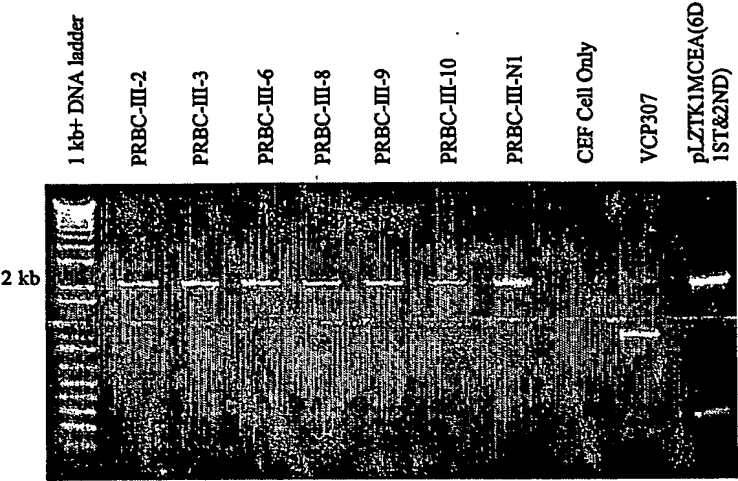
		1301				1350
	mCEA (6D)	TCTCCTGCCA	TGCAGCCTCT	AACCCACCTG	CACAGTATTC	TTGGCTGATT
5	mCEA (6D, 1st&2nd)	<u>TTCT</u> TGCCA	TGCAGC <u>ATCC</u>	AACCC <u>CCCTG</u>	CACAGT <u>ACTC</u>	<u>CTGGCTGATT</u>
		1351				1400
	mCEA (6D)	GATGGGAACA	TCCAGCAACA	CACACAAGAG	CTCTTTATCT	CCAACATCAC
	mCEA (6D, 1st&2nd)	GATGG <u>AAACA</u>	<u>TTCAGCAGCA</u>	<u>TACTCAAGAG</u>	<u>TTATTTATAA</u>	<u>GCAACATAAC</u>
10		1401				1450
	mCEA (6D)	TGAGAAGAAC	AGCGGACTCT	ATACCTGCCA	GGCCAATAAC	TCAGCCAGTG
	mCEA (6D, 1st&2nd)	TGAGAAGAAC	AGCGGACTCT	ATAC <u>TTGCCA</u>	GGCCAATAAC	TCAGCCAGTG
		1451				1500
15	mCEA (6D)	GCCACAGCAG	GACTACAGTC	AAGACAATCA	CAGTCTCTGC	GGAGCTGCCC
	mCEA (6D, 1st&2nd)	<u>GTCACAGCAG</u>	GACTACAG <u>TT</u>	<u>AAAACAATAA</u>	<u>CTGTTTCCGC</u>	GGAGCTGCCC
		1501				1550
	mCEA (6D)	AAGCCCTCCA	TCTCCAGCAA	CAACTCCAAA	CCCGTGGAGG	ACAAGGATGC
20	mCEA (6D, 1st&2nd)	AAGCCCTCCA	TCTCCAGCAA	CAACTCCAAA	CCCGTGGAGG	ACAAGGATGC
		1551				1600
	mCEA (6D)	TGTGGCCTTC	ACCTGTGAAC	CTGAGGCTCA	GAACACAACC	TACCTGTGGT
25	mCEA (6D, 1st&2nd)	TGTGGCCTTC	ACCTGTGAAC	CTGAGGCTCA	GAACACAACC	TACCTGTGGT
		1601				1650
	mCEA (6D)	GGGTAAATGG	TCAGAGCCTC	CCAGTCAGTC	CCAGGCTGCA	GCTGTCCAAT
	mCEA (6D, 1st&2nd)	GGGTAAATGG	TCAGAGCCTC	CCAGTCAGTC	CCAGGCTGCA	GCTGTCCAAT
30		1651				1700
	mCEA (6D)	GGCAACAGGA	CCCTCACTCT	ATTCAATGTC	ACAAGAAATG	ACGCAAGAGC
	mCEA (6D, 1st&2nd)	GGCAACAGGA	CCCTCACTCT	ATTCAATGTC	ACAAGAAATG	ACGCAAGAGC
		1701				1750
35	mCEA (6D)	CTATGTATGT	GGAATCCAGA	ACTCAGTGAG	TGCAAACCGC	AGTGACCCAG
	mCEA (6D, 1st&2nd)	CTATGTATGT	GGAATCCAGA	ACTCAGTGAG	TGCAAACCGC	AGTGACCCAG
		1751				1800
	mCEA (6D)	TCACCCTGGA	TGTCCTCTAT	GGGCCGGACA	CCCCCATCAT	TTCCCCCCCCA
40	mCEA (6D, 1st&2nd)	TCACCCTGGA	TGTCCTCTAT	GGGCCGGACA	CCCCCATCAT	TTCCCCCCCCA
		1801				1850
	mCEA (6D)	GACTCGTCTT	ACCTTTCGGG	AGCGGACCTC	AACCTCTCCT	GCCACTCGGC
45	mCEA (6D, 1st&2nd)	GACTCGTCTT	ACCTTTCGGG	AGCGGACCTC	AACCTCTCCT	GCCACTCGGC
		1851				1900
	mCEA (6D)	CTCTAACCCA	TCCCCGCAGT	ATTCTTGCGG	TATCAATGGG	ATACCGCAGC
	mCEA (6D, 1st&2nd)	CTCTAACCCA	TCCCCGCAGT	ATTCTTGCGG	TATCAATGGG	ATACCGCAGC
50		1901				1950
	mCEA (6D)	AACACACACA	AGTTCTCTTT	ATCGCCAAAA	TCACGCCAAA	TAATAACGGG
	mCEA (6D, 1st&2nd)	AACACACACA	AGTTCTCTTT	ATCGCCAAAA	TCACGCCAAA	TAATAACGGG

12/29

FIGURE 9D

		1951				2000
	mCEA (6D)	ACCTATGCCT	GTTTTGTCTC	TAACTTGGCT	ACTGGCCGCA	ATAATTCCAT
5	mCEA (6D, 1st&2nd)	ACCTATGCCT	GTTTTGTCTC	TAACTTGGCT	ACTGGCCGCA	ATAATTCCAT
		2001				2050
	mCEA (6D)	AGTCAAGAGC	ATCACAGTCT	CTGCATCTGG	AACTTCTCCT	GGTCTCTCAG
10	mCEA (6D, 1st&2nd)	AGTCAAGAGC	ATCACAGTCT	CTGCATCTGG	AACTTCTCCT	GGTCTCTCAG
		2051				2100
	mCEA (6D)	CTGGGGCCAC	TGTCGGCATC	ATGATTGGAG	TGCTGGTTGG	GGTTGCTCTG
	mCEA (6D, 1st&2nd)	CTGGGGCCAC	TGTCGGCATC	ATGATTGGAG	TGCTGGTTGG	GGTTGCTCTG
15		2101				
	mCEA (6D)	ATATAG				
	mCEA (6D, 1st&2nd)	ATATAG				

FIGURE 10



14/29

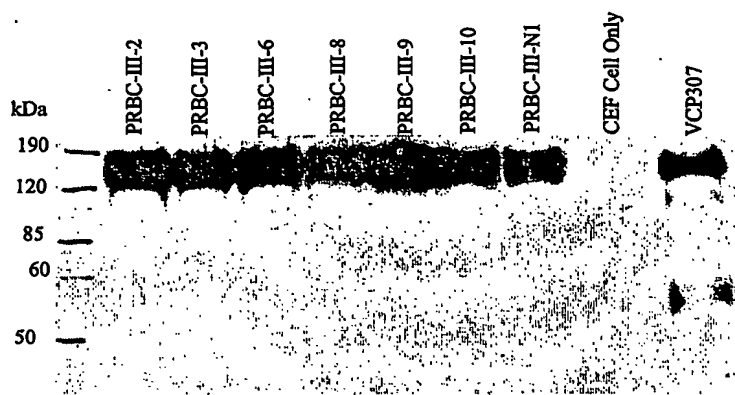
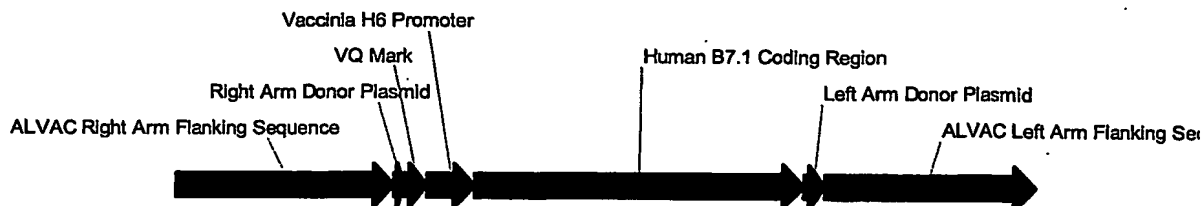
FIGURE 11

FIGURE 12

ALVAC Right Arm Flanking Sequence

1 TTAGATTGTG TTATTCATTA CATAGACGCT GCTAAATCTA CTATCGATT
AATCTAACAC AATAAGTAAT GTATCTGCGA CGATTTAGAT GATAGCTAAA

ALVAC Right Arm Flanking Sequence

51 AGAGATAGTA TCTCTACTAC CCACAAAAAG AACTAAAGAC GCCATAGTGT
TCTCTATCAT AGAGATGATG GGTGTTTTTC TTGATTICTG CGGTATCACA

ALVAC Right Arm Flanking Sequence

101 ACTGGCCTAT AATAAAAGAC GCGTTGATAA GAGCTGTTCT GGAACGTGGT
TGACCGGATA TTATTTTCTG CGCAACTATT CTCGACAAGA CCTTGCACCA

ALVAC Right Arm Flanking Sequence

151 GTTAAACTTA GAATACTACT AGGTTATTGG AAAAAGACCG ATATTATCTC
CAATTTGAAT CTTATGATGA TCCAATAACC TTTTCTGGC TATAATAGAG

ALVAC Right Arm Flanking Sequence

201 TAAAGCTTCT ATCAAAAGTC TTAATGAGTT AGGTGTAGAT AGTATAGATA
ATTTCGAAGA TAGTTTTTCAG AATTACTCAA TCCACATCTA TCATATCTAT

ALVAC Right Arm Flanking Sequence

251 TTACTACAAA GGTATTCATA TTTCTATCA ATTCTAAAGT AGATGATATT
AATGATGTTT CCATAAGTAT AAAGGATAGT TAAGATTTC. TCTACTATAA

ALVAC Right Arm Flanking Sequence

301 AATAACTCAA AGATGATGAT AGTAGATAAT AGATACGCTC ATATAATGAC
TTATTGAGTT TCTACTACTA TCATCTATTA TCTATGCGAG TATATTACTG

ALVAC Right Arm Flanking Sequence

351 TGCAAATTTG GACGGTTCAC ATTTTAATCA TCACGCGTTC ATAAGTTTCA
ACGTTTAAAC CTGCCAAGTG TAAATTAGT AGTGCGCAAG TATTCAAAGT

16/29

ALVAC Right Arm Flanking Sequence

~~~~~  
401 ACTGCATAGA TCAAAATCTC ACTAAAAAGA TAGCCGATGT ATTTGAGAGA  
TGACGTATCT AGTTTTAGAG TGATTTTCT ATCGGCTACA TAAACTCTCT

## ALVAC Right Arm Flanking Sequence

~~~~~  
451 GATTGGACAT CTAACCTACGC TAAAGAAATT ACAGTTATAA ATAATACATA
CTAACCTGTA GATTGATGCG ATTTCTTTAA TGTCAATATT TATTATGTAT

ALVAC Right Arm Flanking Sequence

~~~~~  
501 ATGGATTTTG TTATCATCAG TTATATTTAA CATAAGTACA ATAAAAAGTA  
TACCTAAAAC AATAGTAGTC AATATAAATT GTATTCATGT TATTTTTCAT

## Right Arm Donor Plasmid

## ALVAC Right Arm Flanking Sequence

~~~~~  
551 TTAAATAAAA ATACTACTT ACGAAAAAAT GACTAATTAG CTATAAAAAC
AATTTATTTT TATGAATGAA TGCTTTTTTA CTGATTAATC GATATTTTGT

VQ Mark

Right Arm Donor Plasmid

~~~~~  
601 CCGGGTTAAT TAATTAGTTA TTAGACAAGG TGAAAACGAA ACTATTTGTA  
GGCCCAATTA ATTAATCAAT AATCTGTTC ACTTTTGCTT TGATAAACAT

## VQ Mark

## Vaccinia H6 Promoter

~~~~~  
651 GCTTAATTAA TTAGAGCTTC TTTATTCTAT ACTTAAAAAG TGAAAATAAA
CGAATTAATT AATCTCGAAG AAATAAGATA TGAATTTTTC ACTTTTATTT

Vaccinia H6 Promoter

~~~~~  
701 TACAAAGGTT CTTGAGGGTT GTGTTAAATT GAAAGCGAGA AATAATCATA  
ATGTTTCCAA GAACTCCCAA CACAATTTAA CTTTCGCTCT TTATTAGTAT

## Human B7.1 Coding Region

## Vaccinia H6 Promoter

~~~~~  
751 AATTATTTCA TTATCGGAT ATCCGTTAAG TTTGTATCGT AATGGGCCAC
TTAATAAAGT AATAGCGCTA TAGGCAATTC AAACATAGCA TTACCCGGTG

Human B7.1 Coding Region

~~~~~  
801 ACACGGAGGC AGGGAACATC ACCATCCAAG TGTCCATACC TCAATTTCTT  
TGTGCCTCCG TCCCTTGTAG TGGTAGGTTT ACAGGTATGG AGTTAAAGAA

## Human B7.1 Coding Region

~~~~~  
851 TCAGCTCTTG GTGCTGGCTG GTCTTTCTCA CTTCTGTTCA GGTGTTATCC
AGTCGAGAAC CACGACCGAC CAGAAAGAGT GAAGACAAGT CCACAATAGG

Human B7.1 Coding Region

901 ACGTGACCAA GGAAGTGAAA GAAGTGGCAA CGCTGTCCTG TGGTCACAAT
TGCACCTGGTT CCTTCACTTT CTTCAACCGTT GCGACAGGAC ACCAGTGTTA

Human B7.1 Coding Region

951 GTTCTCTGTTG AAGAGCTGGC ACAAACCTCGC ATCTACTGGC AAAAGGAGAA
CAAAGACAAC TTCTCGACCG TGTGAGGCG TAGATGACCG TTTTCTCTT

Human B7.1 Coding Region

1001 GAAAATGGTG CTGACTATGA TGTCTGGAGA CATGAATATA TGGCCCAGAT
CTTTTACCAC GACTGATACT ACAGACCTCT GTACTTATAT ACCGGGCTCA

Human B7.1 Coding Region

1051 ACAAGAACCG GACCATCTTT GATATCACTA ATAACCTCTC CATTGTGATC
TGTTCTTGGC CTGGTAGAAA CTATAGTGAT TATTGGAGAG GTAACACTAG

Human B7.1 Coding Region

1101 CTGGCTCTGC GCCCATCTGA CGAGGGCACA TACGAGTGTG TTGTTCTGAA
GACCGAGACG CGGGTAGACT GCTCCCGTGT ATGCTCACAC AACAAGACTT

Human B7.1 Coding Region

1151 GTATGAAAAA GACGCTTCA AGCGGGAACA CCTGGCTGAA GTGACGTTAT
CATACTTTTT CTGCGAAAGT TCGCCCTTGT GGACCGACTT CACTGCAATA

Human B7.1 Coding Region

1201 CAGTCAAAGC TGACTTCCCT ACACCTAGTA TATCTGACTT TGAAATTCCA
GTCAGTTTCG ACTGAAGGGA TGTGGATCAT ATAGACTGAA ACTTTAAGGT

Human B7.1 Coding Region

1251 ACTTCTAATA TTAGAAGGAT AATTGCTCA ACCTCTGGAG GTTTTCCAGA
TGAAGATTAT AATCTTCCTA TTAAACGAGT TGGAGACCTC CAAAAGGTCT

Human B7.1 Coding Region

1301 GCCTCACCTC TCCTGGTTGG AAAATGGAGA AGAATTAAAT GCCATCAACA
CGGAGTGGAG AGGACCAACC TTTTACCTCT TCTTAATTTA CGGTAGTTGT

Human B7.1 Coding Region

1351 CAACAGTTTC CCAAGATCCT GAAACTGAGC TCTATGCTGT TAGCAGCAAA
GTTGTCAAAG GGTTCTAGGA CTTTGACTCG AGATACGACA ATCGTCGTTT

Human B7.1 Coding Region

1401 CTGGATTTC AATATGACAAC CAACCACAGC TTCATGTGTC TCATCAAGTA
GACCTAAAGT TATACTGTTG GTTGGTGTG AAGTACACAG AGTAGTTCAT

18/29

Human B7.1 Coding Region

~~~~~  
1451 TGGACATTTA AGAGTGAATC AGACCTTCAA CTGGAATACA ACCAAGCAAG  
ACCTGTAAAT TCTCACTTAG TCTGGAAGTT GACCTTATGT TGGTTCGTTC

## Human B7.1 Coding Region

~~~~~  
1501 AGCATTTTCC TGATAACCTG CTCCCATCCT GGGCCATTAC CTTAATCTCA
TCGTAAAAGG ACTATTGGAC GAGGGTAGGA CCCGGTAATG GAATTAGAGT

Human B7.1 Coding Region

~~~~~  
1551 GTAAATGGAA TTTTCGTGAT ATGCTGCCTG ACCTACTGCT TTGCCCCACG  
CATTTACCTT AAAAGCACTA TACGACGGAC TGGATGACGA AACGGGGTGC

## Human B7.1 Coding Region

~~~~~  
1601 CTGCAGAGAG AGAAGGAGGA ATGAGAGATT GAGAAGGGAA AGTGACGTC
GACGTCTCTC TCTTCTCCT TACTCTCTAA CTCTTCCCTT TCACATGCAG

Left Arm Donor Plasmid

~~~~~  
Human B7.1 Coding Region

~~~~~  
1651 CTGTATAATT TTTATCTCGA GCCCGGGAAG CTTGAATTCT TTTTATTGAT
GACATATTAA AAATAGAGCT CGGGCCCTTC GAACTTAAGA AAAATAACTA

~~~~~  
ALVAC Left Arm Flanking Sequence~~~~~  
Left Arm Donor Plasmid

~~~~~  
1701 TAACTAGTCA AATGAGTATA TATAATTGAA AAAGTAAAAT ATAAATCATA
ATTGATCAGT TTAATCATAT ATATTAACTT TTTCATTTTA TATTTAGTAT

~~~~~  
ALVAC Left Arm Flanking Sequence

~~~~~  
1751 TAATAATGAA ACGAAATATC AGTAATAGAC AGGAACTGGC AGATTCTTCT
ATTATTACTT TGCTTTATAG TCATTATCTG TCCTTGACCG TCTAAGAAGA

~~~~~  
ALVAC Left Arm Flanking Sequence

~~~~~  
1801 TCTAATGAAG TAAGTACTGC TAAATCTCCA AAATTAGATA AAAATGATAC
AGATTACTTC ATTCATGACG ATTTAGAGGT TTTAATCTAT TTTTACTATG

~~~~~  
ALVAC Left Arm Flanking Sequence

~~~~~  
1851 AGCAAATACA GCTTCATTCA ACGAATTACC TTTTAATTTT TTCAGACACA
TCGTTTATGT CGAAGTAAGT TGCTTAATGG AAAATTAAAA AAGTCTGTGT

~~~~~  
ALVAC Left Arm Flanking Sequence

~~~~~  
1901 CCTTATTACA AACTAACTAA GTCAGATGAT GAGAAAGTAA ATATAAATTT
GGAATAATGT TTGATTGATT CAGTCTACTA CTCTTTCATT TATATTTAA

ALVAC Left Arm Flanking Sequence

1951 AACTTATGGG TATAATATAA TAAAGATTCA TGATATTAAT AATTTACTTA
TTGAATACCC ATATTATATT ATTTCTAAGT ACTATAATTA TTAAATGAAT

ALVAC Left Arm Flanking Sequence

2001 ACGATGTTAA TAGACTTATT CCATCAACCC CTTCAAACCT TTCTGGATAT
TGCTACAATT ATCTGAATAA GGTAGTTGGG GAAGTTTGGA AAGACCTATA

ALVAC Left Arm Flanking Sequence

2051 TATAAAATAC CAGTTAATGA TATTAAAATA GATTGTTTAA GAGATGTAAA
ATATTTTATG GTCAATTACT ATAATTTTAT CTAACAAATT CTCTACATTT

ALVAC Left Arm Flanking Sequence

2101 TAATTATTTG GAGGTAAAGG ATATAAAATT AGTCTATCTT TCACATGGAA
ATTAATAAAC CTCCATTTCC TATATTTTAA TCAGATAGAA AGTGTACCTT

ALVAC Left Arm Flanking Sequence

2151 ATGAATTACC TAATATTAAT AATTATGATA GGAATTTTTT AGGATTTACA
TACTTAATGG ATTATAATTA TTAATACTAT CCTTAAAAAA TCCTAAATGT

ALVAC Left Arm Flanking Sequence

2201 GCTGTTATAT GTATCAACAA TACAGGCAGA TCTATGGTTA TGGTAAACAA
CGACAATATA CATAGTTGTT ATGTCCGTCT AGATACCAAT ACCATTTTGT

ALVAC Left Arm Flanking Sequence

2251 CTGTAACGGG AAGCAGCAT
GACATTGCCC TTCGTCGTA

FIGURE 13

C3R Arm

1 ATATTATTAA AACTATTAGA TAACATAGCT TTATGTAAAG GAGTATTTCC
TATAATAATT TTGATAATCT ATTGTATCGA AATACATTTC CTCATAAAGG

C3R Arm

51 AGATAACTTA GCTTTAGCAT TTACGTAAGC ACCGTGGTCA AGTAAGAGTT
TCTATTGAAT CGAAATCGTA AATGCATTTCG TGGCACCAGT TCATTCTCAA

C3R Arm

101 TAACAAATTC TGTTTTTCATA GAACTAACTG CCATGTATAG AGGAGTGAAA
ATTGTTTAAAG ACAAAGTAT CTTGATTGAC GGTACATATC TCCTCACTTT

C3R Arm

151 CCTTTATGAT TATAGACGTT TACATAGCAA CCATATAATA AGATCGCATT
GGAAATACTA ATATCTGCAA ATGTATCGTT GGTATATTAT TCTAGCGTAA

C3R Arm

201 CAGTATATTA ATATCTTTCA TTTCTATAGC TATGTGAATA ACATGTTTAT
GTCATATAAT TATAGAAAAGT AAAGATATCG ATACACTTAT TGTACAAATA

C3R Arm

251 CTAATCCTAC CAACTTTGTA TCAGTACCGT ACTTCAGTAA TAAGTTTACT
GATTAGGATG GTTGAAACAT AGTCATGGCA TGAAGTCATT ATTCAAATGA

C3R Arm

301 ATAGTTTTGT TTTTAGATGC AACAGCTATA TTTAGAACGG TATCTATATG
TATCAAAACA AAAATCTACG TTGTCGATAT AAATCTTGCC ATAGATATAC

C3R Arm

~~~~~  
351 ATTATTAACC ACATTAACAT TAGATCCTCT TTCTAAAAGT GTCTTTGTTG  
TAATAATTGG TGTAATTGTA ATCTAGGAGA AAGATTTTCA CAGAAACAAC

## C3R Arm

~~~~~  
401 TTTCGATATC GTTACGTGAA ACAGCGTAAT GTAAGGGACT GCCCATAACG
AAAGCTATAG CAATGCACTT TGTCGCATTA CATTCCCTGA CGGGTATGTC

C3R Arm

~~~~~  
451 TCATCTATTA CGTTTATATC AGCTCCTAGA TTAAACAGAA GTGCTGTTAC  
AGTAGATAAT GCAAATATAG TCGAGGATCT AAATTGTCTT CACGACAATG

## C3R Arm

~~~~~  
501 ATCTTTTCTT CTATTAATTA CCGAATGATG TAATGGGGTT TTACCTAAAT
TAGAAAAGAA GATAATTAAT GGCTTACTAC ATTACCCCAA AATGGATTTA

C3R Arm

~~~~~  
551 CATCTTGTTT GTTTATAGGC ACTCCGTGAT TTATAAGTAA CGCTATTATA  
GTAGAACAAG CAAATATCCG TGAGGCACTA AATATTCATT GCGATAATAT

## C3R Arm

~~~~~  
601 TCGTAACTAC AATTATTTT AAGTGCCTTT ATGAGATACT GTTTATGCAA
AGCATTGATG TTAATAAAAA TTCACGGAAA TACTCTATGA CAAATACGTT

C3R Arm

~~~~~  
651 AAATAAACTT TTATCTATTT TAATACTATT ATCTAACAAT ATCCTAATTA  
TTTATTTGAA AATAGATAAA ATTATGATAA TAGATTGTTA TAGGATTAAT

## C3R Arm

~~~~~  
701 AATCTATATT CTTATACTTT ATAGCGTAAT GTAACGGAGT TTCAAAATTT
TTAGATATAA GAATATGAAA TATCGCATTA CATTGCCTCA AAGTTTTTAAA

C3R Arm

~~~~~  
751 CTAGTTTGTA TATTAAGATC AATATTAAAA TCTATAAATA TTTTATACAT  
GATCAAACAT ATAATCTAG TTATAATTTT AGATATTTAT AAAATATGTA

## C3R Arm

~~~~~  
801 ATCATCAGAT ATCTTATCAT ACAGTACATC GTAATAATTT AGAAAGAATC
TAGTAGTCTA TAGAATAGTA TGTCATGTAG CATTATTAAA TCTTTCTTAG

C3R Arm

~~~~~  
851 TATTACAATT AACACCTTTT TTTAATAAAT ATCTAGTTAA TGACTTATTG  
ATAATGTTAA TTGTGGAAAA AAATTATTTA TAGATCAATT ACTGAATAAC

## C3R Arm

901 TTTCTATATA CAGAAATATA TAACGGACTA TTTCCAGAAT GTATCTGTTT  
AAAGATATAT GTCCTTTATAT ATTGCCTGAT AAAGGTCTTA CATAGACAAG

## C3R Arm

951 TATGTCAGCG CCAGAATCTA TTAGTAGTTT AGCAATTTCT GTATTATCTA  
ATACAGTCGC GGTCTTAGAT AATCATCAAA TCGTTAAAGA CATAATAGAT

## C3R Arm

1001 AACTAGCAGC TTTATGAAGA GGAGGATTTT TACATTTTAA AATATCGGCA  
TTGATCGTCG AAATACTTCT CCTCCTAAAA ATGTAAAAAT TTATAGCCGT

## C3R Arm

1051 CCGTGTTCTA GTAATAATTT TACCATTCTT ATATCAGAAA TACTTACGGC  
GGCACAAGAT CATTATTAAA ATGGTAAAGA TATAGTCTTT ATGAATGCCG

## C3R Arm

1101 TAAATACAAA GACGTTGATA GTATATTTAC GTTATTGTAT TTGCATTTTT  
ATTTATGTTT CTGCAACTAT CATATAAATG CAATAACATA AACGTAAAAA

## C3R Arm

1151 TAAGTATATA CCTTACTAAA TTTATATCTC TATACCTTAT AGCTTTATGC  
ATTCATATAT GGAATGATTT AAATATAGAG ATATGGAATA TCGAAATACG

## C3R Arm

1201 AGTTCATTTA TAAGTCTTCC ATTACTCATT TCTGGTAATG AAGTATTATA  
TCAAGTAAAT ATTCAGAAGG TAATGAGTAA AGACCATTAC TTCATAATAT

## C3R Arm

1251 TATCATTATG ATATTATCTC TATTTTATTC TAATAAAAAAC CGTTATCATG  
ATAGTAATAC TATAATAGAG ATAAAAAAG ATTATTTTTC GCAATAGTAC

## C3R Arm

1301 TTATTTATTA TTTGTTATAA TTATACTATT TAATAAATTA TACCAAATAC  
AATAAATAAT AAACAATATT AATATGATAA ATTATTTAAT ATGGTTTATG

## C3R Arm

1351 TTAGATACTT ATTAATACCA TCCTAGAACT TGTATTTCTT GCCCCCTAAA  
AATCTATGAA TAATTATGGT AGGATCTTGA ACATAAAGAA CGGGGGATTT

## C3R Arm

1401 CTTGGACATG CACTCCATTA GCGGTTTCTT GTTTTCGACA TCGTCCTCCT  
GAACCTGTAC GTGAGGTAAT CCGCAAAGAA CAAAAGCTGT AGCAGGAGGA

## C3R Arm

~~~~~  
1451 TAACATATCC TACTGTTATG TGAGGATTCC ACGGATTATC TACTGTGATA
ATTGTATAGG ATGACAATAC ACTCCTAAGG TGCCTAATAG ATGACACTAT

C3R Arm

~~~~~  
1501 TCACCAAACA CGTCCTTCGA ACAGGGTACC GCATTCAGCA GAACATTTCT  
AGTGGTTTGT GCAGGAAGCT TGTCCCATGG CGTAAGTCGT CTTGTAAAGA

## C3R Arm

~~~~~  
1551 TAGGGCTCTA AGTTCATCAG ATACCTCCAG TTTCATAACT ACAGCGCATC
ATCCCGAGAT TCAAGTAGTC TATGGAGGTC AAAGTATTGA TGTGCGGTAG

C3R Arm

~~~~~  
1601 CTTTCGCTCC CAACTGTTTA GAGGCGTTAC TCTGAGGAAA ACACATCTCT  
GAAAGCGAGG GTTGACAAAT CTCCGCAATG AGACTCCTTT TGTGTAGAGA

## C3R Arm

~~~~~  
1651 TCTTTACAGA CTATAGAAAT AGTCTGTAAA TCTTGATCAG TTATTTGCTT
AGAAATGTCT GATATCTTTA TCAGACATTT AGAACTAGTC AATAAACGAA

C3R Arm

~~~~~  
1701 TTTGAAATTT TCAAATCTAT CACATTGATC CATATTTGCT ATTCCAAGAG  
AAACTTTAAA AGTTTAGATA GTGTAAGTAG GTATAAACGA TAAGGTTCTC

## C3R Arm

~~~~~  
1751 TTATATGAGG AAAAATATCA CATCCTGTCA TGTATTTTAT TGTAACATTA
AATATACTCC TTTTATAGT GTAGGACAGT ACATAAAATA ACATTGTAAT

C3R Arm

~~~~~  
1801 TTATAATCTG TAACATCAGT ATCTAACCTA ACGTCGTAAA AGTTAACAGA  
AATATTAGAC ATTGTAGTCA TAGATTGGAT TGCAGCATT TCAATTGTCT

## C3R Arm

~~~~~  
1851 TGCCAGTTA CTATAATCCC AAGGAACCTT AACATCTAAT CCCATTAAAA
ACGGGTCAAT GATATTAGGG TTCCTTGGA TTGTAGATTA GGGTAATTTT

C3R Arm

~~~~~  
1901 TAGTATCCTT TCTACTATTT TTTTCATTGG CAAGTATGTG GCTTAGTTTA  
ATCATAGGAA AGATGATAAA AAAAGTAACC GTTCATACAC CGAATCAAAT

## C3R Arm

~~~~~  
1951 CACAAAATTC CTGCCATTTT GTAACGATAG CGAAGCAATA GCTTGTATGC
GTGTTTAAAG GACGGTAAAA CATTGCTATC GCTTCGTTAT CGAACATACG

24/29

H6 promoter
~~~~~  
2001 TTTTATTG ATTAAGTAGT CATAAAATC GGGATCCTC TTTATTCTAT  
AAAAATAAAC TAATTGATCA GTATTTTAG CCCTAGGAAG AAATAAGATA

H6 promoter  
~~~~~  
2051 ACTTAAAAAG TGAAAATAAA TACAAAGGTT CTTGAGGGTT GTGTTAAATT
TGAATTTTC ACTTTTATT ATGTTTCAA GAACTCCCAA CACAATTAA

H6 promoter
~~~~~  
2101 GAAAGCGAGA AATAATCATA AATTATTCA TTATCGCGAT ATCCGTTAAG  
CTTTCGCTCT TTATTAGTAT TTAATAAAGT AATAGCGCTA TAGGCAATTC

MCEA  
~~~~~  
H6 promoter
~~~~~  
2151 TTTGTATCGT AATGGAGTCT CCCTCGGCCC OTCCCCACAG ATGGTGCATC  
AAACATAGCA TTACCTCAGA GGGAGCCGGG GAGGGGTGTC TACCACGTAG

MCEA  
~~~~~  
2201 CCCTGGCAGA GGCTCCTGCT CACAGCCTCA CTTCTAACCT TCTGGAACCC
GGGACCGTCT CCGAGGACGA GTGTCGGAGT GAAGATTGGA AGACCTTGGG

MCEA
~~~~~  
2251 GCCCACCACT GCCAAGCTCA CTATTGAATC CACGCCGTTT AATGTCGCAG  
CGGGTGGTGA CGGTTTCGAGT GATAACTTAG GTGCGGCAAG TTACAGCGTC

MCEA  
~~~~~  
2301 AGGGGAAGGA GGTGCTTCTA CTTGTCCACA ATCTGCCCCA GCATCTTTTT
TCCCCTTCCT CCACGAAGAT GAACAGGTGT TAGACGGGGT CGTAGAAAAA

MCEA
~~~~~  
2351 GGCTACAGCT GGTACAAAGG TGAAAGAGTG GATGGCAACC GTCAAATTAT  
CCGATGTCGA CCATGTTTCC ACTTTCTCAC CTACCGTTGG CAGTTTAATA

MCEA  
~~~~~  
2401 AGGATATGTA ATAGGAACTC AACAAGCTAC CCCAGGGCCC GCATACAGTG
TCCTATACAT TATCCTTGAG TTGTTTCGATG GGGTCCCGGG CGTATGTCAC

MCEA
~~~~~  
2451 GTCGAGAGAT AATATACCCC AATGCATCCC TGCTGATCCA GAACATCATC  
CAGCTCTCTA TTATATGGGG TTACGTAGGG ACGACTAGGT CTTGTAGTAG

MCEA  
~~~~~  
2501 CAGAATGACA CAGGATTCTA CACCCTACAC GTCATAAAGT CAGATCTTGT
GTCTTACTGT GTCCTAAGAT GTGGGATGTG CAGTATTTC A GTCTAGAACA

25/29

MCEA

2551 GAATGAAGAA GCAACTGGCC AGTTCGGGT ATACCCGGAA CTCCCTAAGC
CTTACTTCTT CGTTGACCGG TCAAGGCCCA TATGGGCCTT GAGGGATTCTG

MCEA

2601 CTTCTATTAG CTCCAATAAT AGTAAGCCTG TCGAAGACAA AGATGCCGTC
GAAGATAATC GAGGTTATTA TCATTCCGAC AGCTTCTGTT TCTACGGCAG

MCEA

2651 GCTTTTACAT GCGAGCCCGA AACTCAAGAC GCAACATATC TCTGGTGGGT
CGAAAATGTA CGCTCGGGCT TTGAGTTCTG CGTTGTATAG AGACCACCCA

MCEA

2701 GAACAACCAG TCCCTGCCTG TGTCCTTAG ACTCCAATC AGCAACGGAA
CTTGTTGGTC AGGGACGGAC ACAGGGGATC TGAGGTTGAG TCGTTGCCTT

MCEA

2751 ATAGAACTCT GACCCTGTTT AACGTGACCA GGAACGACAC AGCAAGCTAC
TATCTTGAGA CTGGGACAAA TTGCACTGGT CCTTGCTGTG TCGTTCGATG

MCEA

2801 AAATGCGAAA CCCAAAATCC AGTCAGCGCC AGGAGGTCTG ATTCAGTGAT
TTTACGCTTT GGGTTTTAGG TCAGTCGCGG TCCTCCAGAC TAAGTCACTA

MCEA

2851 TCTCAACGTG CTTTACGGAC CCGATGCTCC TACAATCAGC CCTCTAAACA
AGAGTTGCAC GAAATGCCTG GGCTACGAGG ATGTTAGTCG GGAGATTTGT

MCEA

2901 CAAGCTATAG ATCAGGGGAA AATCTGAATC TGAGCTGTCA TGCCGCTAGC
GTTGATATC TAGTCCCCTT TTAGACTTAG ACTCGACAGT ACGGCGATCG

MCEA

2951 AATCTCCCG CCCAATACAG CTGGTTTGTC AATGGCACTT TCCAACAGTC
TTAGGAGGGC GGGTTATGTC GACCAAACAG TTACCGTGAA AGGTTGTCAG

MCEA

3001 CACCCAGGAA CTGTTCAATC CCAATATTAC CGTGAACAAT AGTGGATCCT
GTGGGTCCTT GACAAGTAAG GGTTATAATG GCACTTGTTA TCACCTAGGA

MCEA

3051 ACACGTGCCA AGCTCACAAT AGCGACACCG GACTCAACCG CACAACCGTG
TGTGCACGGT TCGAGTGTTA TCGCTGTGGC CTGAGTTGGC GTGTTGGCAC

MCEA

~~~~~  
3101 ACGACGATTA CCGTGTATGA GCCACCAAAA CCATTCATAA CTAGTAACAA  
TGCTGCTAAT GGCACATACT CGGTGGTTTT GGTAAGTATT GATCATTGTT

## MCEA

~~~~~  
3151 TTCTAACCCA GTTGAGGATG AGGACGCAGT TGCATTAAC TGTGAGCCAG
AAGATTGGGT CAACTCCTAC TCCTGCGTCA ACGTAATTGA ACACTCGGTC

MCEA

~~~~~  
3201 AGATTCAAAA TACCACTTAT TTATGGTGGG TCAATAACCA AAGTTTGCCG  
TCTAAGTTTT ATGGTGAATA AATACCACCC AGTTATTGGT TTCAAACGGC

## MCEA

~~~~~  
3251 GTTAGCCAC GCTTGCAGTT GTCTAATGAT AACCGCACAT TGACACTCCT
CAATCGGGTG CGAACGTCAA CAGATTACTA TTGGCGTGTA ACTGTGAGGA

MCEA

~~~~~  
3301 GTCCGTTACT CGCAATGATG TAGGACCTTA TGAGTGTGGC ATTCAGAATG  
CAGGCAATGA GCGTTACTAC ATCCTGGAAT ACTCACACCG TAAGTCTTAC

## MCEA

~~~~~  
3351 AATTATCCGT TGATCACTCC GACCCGTGTTA TCCTTAATGT TTTGTATGGC
TTAATAGGCA ACTAGTGAGG CTGGGACAAT AGGAATTACA AAACATACCG

MCEA

~~~~~  
3401 CCAGACGACC CAACTATATC TCCATCATAC ACCTACTACC GTCCCGGCGT  
GGTCTGCTGG GTTGATATAG AGGTAGTATG TGGATGATGG CAGGGCCGCA

## MCEA

~~~~~  
3451 GAAGTTGAGC CTTTCTTGCC ATGCAGCATC CAACCCCCCT GCACAGTACT
CTTGAAGTCG GAAAGAACGG TACGTCGTAG GTTGGGGGGA CGTGTCATGA

MCEA

~~~~~  
3501 CCTGGCTGAT TGATGGAAAC ATTCAGCAGC ATAATAAGA GTTATTTATA  
GGACCGACTA ACTACCTTTG TAAGTCGTCTG TATGAGTTCT CAATAAATAT

## MCEA

~~~~~  
3551 AGCAACATAA CTGAGAAGAA CAGCGGACTC TATACTTGCC AGGCCAATAA
TCGTTGTATT GACTCTTCTT GTCGCCTGAG ATATGAACGG TCCGGTTATT

MCEA

~~~~~  
3601 CTCAGCCAGT GGTCACAGCA GGAATACAGT TAAAACAATA ACTGTTTCCG  
GAGTCGGTCA CCAGTGTCGT CCTGATGTCA ATTTTGTAT TGACAAAGGC

27/29

## MCEA

~~~~~  
3651 CGGAGCTGCC CAAGCCCTCC ATCTCCAGCA ACAACTCCAA ACCCGTGGAG
GCCTCGACGG GTTCGGGAGG TAGAGGTCGT TGTTGAGGTT TGGGCACCTC

MCEA

~~~~~  
3701 GACAAGGATG CTGTGGCCTT CACCTGTGAA CCTGAGGCTC AGAACACAAC  
CTGTTCCCTAC GACACCGGAA GTGGACACTT GGACTCCGAG TCTTGTGTTG

## MCEA

~~~~~  
3751 CTACCTGTGG TGGGTAAATG GTCAGAGCCT CCCAGTCAGT CCCAGGCTGC
GATGGACACC ACCCATTTAC CAGTCTCGGA GGGTCAGTCA GGGTCCGACG

MCEA

~~~~~  
3801 AGCTGTCCAA TGGCAACAGG ACCCTCACTC TATTCAATGT CACAAGAAAT  
TCGACAGGTT ACCGTTGTCC TGGGAGTGAG ATAAGTTACA GTGTTCTTTA

## MCEA

~~~~~  
3851 GACGCAAGAG CCTATGTATG TGGAAATCCAG AACTCAGTGA GTGCAAACCG
CTGCGTTCTC GGATACATAC ACCTTAGGTC TTGAGTCACT CACGTTTGCG

MCEA

~~~~~  
3901 CAGTGACCCA GTCACCCTGG ATGTCCTCTA TGGGCCGGAC ACCCCCATCA  
GTCAGTGGGT CAGTGGGACC TACAGGAGAT ACCCGGCCTG TGGGGGTAGT

## MCEA

~~~~~  
3951 TTTCCCCCCC AGACTCGTCT TACCTTTCGG GAGCGAACCT CAACCTCTCC
AAAGGGGGGG TCTGAGCAGA ATGGAAAGCC CTCGCTTGA GTTGAGAGG

MCEA

~~~~~  
4001 TGCCACTCGG CCTCTAACCC ATCCCCGCAG TATTCTTGGC GTATCAATGG  
ACGGTGAGCC GGAGATTGGG TAGGGGCGTC ATAAGAACCG CATAGTTACC

## MCEA

~~~~~  
4051 GATACCGCAG CAACACACAC AAGTTCTCTT TATCGCCAAA ATCAGCCAA
CTATGGCGTC GTTGTGTGTG TTCAAGAGAA ATAGCGGTTT TAGTGCGGTT

MCEA

~~~~~  
4101 ATAATAACGG GACCTATGCC TGTTTTGTCT CTAAGTTGGC TACTGGCCGC  
TATTATTGCC CTGGATACGG ACAAACAGA GATTGAACCG ATGACCGCGC

## MCEA

~~~~~  
4151 AATAATTCCA TAGTCAAGAG CATCACAGTC TCTGCATCTG GAACTTCTCC
TTATTAAGGT ATCAGTTCTC GTAGTGTCAG AGACGTAGAC CTTGAAGAGG

28/29

MCEA

~~~~~  
4201 TGGTCTCTCA GCTGGGGCCA CTGTCGGCAT CATGATTGGA GTGCTGGTTG  
ACCAGAGAGT CGACCCCGGT GACAGCCGTA GTACTAACCT CACGACCAAC

## MCEA

~~~~~  
4251 GGGTTGCTCT GATATAGTTT TTATCTCGAG GAATTCCTGC AGCCCGGGTT
CCCAACGAGA CTATATCAAA AATAGAGCTC CTTAAGGACG TCGGGCCCAA

C3L Arm

~~~~~  
4301 TTTATAGCTA ATTAGTCAAA TGTGAGTTAA TATTAGTATA CTACATTACT  
AAATATCGAT TAATCAGTTT AACTCAATT ATAATCATAT GATGTAATGA

## C3L Arm

~~~~~  
4351 AATTTATTAC ATATTCATTT ATATCAATCT AGTAGCATT AGCTTTTATA
TTAAATAATG TATAAGTAAA TATAGTTAGA TCATCGTAAA TCGAAAATAT

C3L Arm

~~~~~  
4401 AAACAATATA ACTGAATAGT ACATACTTTA CTAATAAGTT ATAAATAAGA  
TTTGTTATAT TGACTTATCA TGTATGAAAT GATTATTCAA TATTTATTCT

## C3L Arm

~~~~~  
4451 GATACATATT TATAGTATTT TACTTTCTAC ACTGAATATA ATAATATAAT
CTATGTATAA ATATCATAAA ATGAAAGATG TGACTTATAT TATTATATTA

C3L Arm

~~~~~  
4501 TATACAAATA TAATTTTAA TACTATATAG TATATAACTG AAATAAATA  
ATATGTTTAT ATTAAAAATT ATGATATATC ATATATTGAC TTTATTTTAT

## C3L Arm

~~~~~  
4551 CCAGTGTAAT ATAGTTATTA TACATTTATA CCACATCAAA GATGAGTTAT
GGTCACATTA TATCAATAAT ATGTAAATAT GGTGTAGTTT CTACTCAATA

C3L Arm

~~~~~  
4601 AACATCAGTG TCACTGTTAG CAACAGTAGT TATACGATGA GTAGTTACTC  
TTGTAGTCAC AGTGACAATC GTTGTCATCA ATATGCTACT CATCAATGAG

## C3L Arm

~~~~~  
4651 TCGTATGGCG TTAGTATGTA TGTATCTTCT AGTTTCTTA GTAGGCATTA
AGCATACCGC AATCATACAT ACATAGAAGA TCAAAAGAAT CATCCGTAAT

C3L Arm

~~~~~  
4701 TAGGAAACGT CAAGCTTATA AGGTTATTAA TGGTATCTAG AAATATATCT  
ATCCTTTGCA GTTCGAATAT TCCAATAATT ACCATAGATC TTTATATAGA

## C3L Arm

~~~~~  
4751 ATTATACCGT TTCTCAACTT GGAATAGCC GATTGCTGT TTGTGATATT
TAATATGGCA AAGAGTTGAA CCCTTATCGG CTAAACGACA AACACTATAA

C3L Arm

~~~~~  
4801 CATACCTTTA TACATTATAT ACATACTAAG TAATTTCCAT TGGCATTTTG  
GTATGGAAAT ATGTAATATA TGTATGATTC ATTAAAGGTA ACCGTAAAAC

## C3L Arm

~~~~~  
4851 GTAAAGCACT TTGTAAAATT AGTTCCTTCT TTTTACTTC TAACATGTTT
CATTTTCGTGA AACATTTTAA TCAAGAAAGA AAAAATGAAG ATTGTACAAA

C3L Arm

~~~~~  
4901 GCAAGTATAT TTTTAATAAC TGTAATAAGC GTATATAGAT ATGTAAAAAT  
CGTTCATATA AAAATTATTG ACATTATTCG CATATATCTA TACATTTTTA

## C3L Arm

~~~~~  
4951 TACCCTTCCT GGATTTACCT ATAAATATGT TAACATTAGA AATATGTACA
ATGGGAAGGA CCTAAATGGA TATTTATACA ATTGTAATCT TTATACATGT

C3L Arm

~~~~~  
5001 TTACTATATT TTTCATATGG ATTATTTCTA TTATACTAGG GATTCCTGCT  
AATGATATAA AAAGTATACC TAATAAAGAT AATATGATCC CTAAGGACGA

## C3L Arm

~~~~~  
5051 CTTTACTTTA GAAATACTAT CGTAACAAA AATAACGACA CGCTGTGTAT
GAAATGAAAT CTTTATGATA GCATTGTTTT TTATTGCTGT GCGACACATA

C3L Arm

~~~~~  
5101 TAATCATTAT CATGATAATA GAGAAATTGC TGAATTGATT TACAAAGTTA  
ATTAGTAATA GTACTATTAT CTCTTTAACG ACTTAACATA ATGTTTCAAT

## C3L Arm

~~~~~  
5151 TTATCTGTAT CAGATTTATT TTAGGATACC TACTACCTAC GATAATTATA
AATAGACATA GTCTAAATAA AATCCTATGG ATGATGGATG CTATTAATAT

C3L Arm

~~~~~  
5201 CTCGTATGCT ATACGTTACT GATCTACAGA ACTAACAATG CATGTCGACG  
GAGCATACGA TATGCAATGA CTAGATGTCT TGATTGTTAC GTACAGCTGC

## C3L Arm

~~~~~  
5251 CGGCCGCAA
GCCGGCGTT